

5' NET AAA TCA GCC TCT TGC CCC ATT GCT CTT TGC AGG GGT AGA AGA AGG AAG TGT

AGC GGG GTA AGG AAT GCA CCG TCA GGG TCT CTC ACA ACC CTT TCC CAG CTC TCC

TCC CCA ACA AAC AGT ACC TGG GAT GGA GCC CTA GGG TAA TCG CAG CCA CGG GAT

GGG TCG AGG TGA CAG GCT TCA GGG ACC ACA CTT CGG CCT TTG CCC GAC CTT CCA

CAA CTT AAG CGA AGA GAG GCC ACC AGC CGT AAC AGG GCG TTA AAG CCC AGG GGA

AGA TTG GTC CTT ATG ACT TGC TGC CTT CCA GCC CTC AGA TTC ATC GCT ACC CCG

M T C C L P A L R F I A T P

AGG CTA AGC GCC ATG CCT CAT ATT GAC AAC GAT GTG AAA CTG GAC TTC AAG GAT

R L S A M P H I D N D V K L D F K D

GTC CTT TTG AGG CCC AAA CGC AGT ACC CTT AAG TCT CGA AGT GAG GTG GAT CTC

V L L R P K R S T L K S R S E V D L

ACA AGA TCC TTT TCA TTT CGG AAC TCA AAG CAG ACA TAC TCT GGG GTT CCC ATC

T R S F S F R N S K Q T Y S G V P I

ATT GCT GCC AAT ATG GAT ACT GTG GGC ACC TTT GAG ATG GCC AAG GTT CTC TGT

I A A N M D T V G T F E M A K V L C

AAG TTC TCT CTC TTC ACT GCT GTC CAT AAG CAC TAT AGC CTC GTT CAG TGG CAA

K F S L F T A V H K H Y S L V Q W Q

GAG TTT GCT GGC CAG AAT CCT GAC TGT CTT GAG CAT CTG GCT GCC AGC TCA GGC

E F A G Q N P D C L E H L A A S S G

ACA GGC TCT TCT GAC TTT GAG CAG CTG GAA CAG ATC CTG GAA GCT ATT CCC CAG

T G S S D F E Q L E Q I L E A I P Q

FIGURE 1A

-	711	720	729	738	747	756
GTG AAG TAT ATA TGC CTG GAT GTG GCA AAT GGC TAC TCT GAA CAC TTT GTT GAA						
V K Y I C L D V A N G Y S E H F V E						
765	774	783	792	801	810	
TTT GTA AAA GAT GTA CGG AAG CGC TTC CCC CAG CAC ACC ATC ATG GCA GGG AAT						
F V K D V R K R F P Q H T I M A G N						
819	828	837	846	855	864	
GTG GTA ACA GGA GAG ATG GTA GAA GAG CTC ATC CTT TCT GGG GCT GAC ATC ATC						
V V T G E M V E E L I L S G A D I I						
873	882	891	900	909	918	
AAA GTG GGA ATT GGG CCA GGC TCT GTG TGT ACT ACT CGG AAG AAA ACT GGA GTG						
K V G I G P G S V C T T R K K T G V						
927	936	945	954	963	972	
GGG TAT CCA CAG CTC AGC GCA GTG ATG GAG TGT GCA GAT GCT GCT CAT GGC CTC						
G Y P Q L S A V M E C A D A A H G L						
981	990	999	1008	1017	1026	
AAA GGC CAC ATC ATT TCA GAT GGA GGT TGC AGC TGT CCT GGG GAT GTG GCC AAG						
K G H I I S D G G C S C P G D V A K						
1035	1044	1053	1062	1071	1080	
GCT TTT GGG GCA GGA GCT GAC TTC GTG ATG CTG GGT GGC ATG CTG GCT GGG CAC						
A F G A G A D F V M L G G M L A G H						
1089	1098	1107	1116	1125	1134	
AGT GAG TCA GGT GGT GAG CTC ATC GAG AGG GAT GGC AAG AAG TAC AAG CTC TTC						
S E S G G E L I E R D G K K Y K L F						
1143	1152	1161	1170	1179	1188	
TAT GGA ATG AGT TCT GAA ATG GCC ATG AAG AAG TAT GCT GGG GGC GTG GCT GAG						
Y G M S S E M A M K K Y A G G V A E						
1197	1206	1215	1224	1233	1242	
TAC AGA GCC TCA GAG GGA AAG ACA GTG GAA GTT CCT TTT AAA GGA GAT GTG GAA						
Y R A S E G K T V E V P F K G D V E						
1251	1260	1269	1278	1287	1296	
CAT ACC ATC CGA GAC ATC CTA GGA GGG ATC CGC TCT ACG TGT ACC TAT GTG GGA						
H T I R D I L G G I R S T C T Y V G						
1305	1314	1323	1332	1341	1350	
GCA GCT AAG CTC AAA GAG TTG AGC AGG AGA ACT ACC TTC ATC CGA GTC ACC CAG						
A A K L K E L S R R T T F I R V T Q						
1359	1368	1377	1386	1395	1404	
CAG GTG AAT CCA ATC TTC AGT GAG GCG TGC TAG ACC TGA GCA GTT CTA CCC TCC						
Q V N P I F S E A C						

FIGURE 1B

1413	1422	1431	1440	1449	1458
CAA GGC ACC AGT ACT CTA CCA TGG GGC ATC CCA AGT GGG GTC CTC ACC CAT CCC					
1467	1476	1485	1494	1503	1512
AGC TAC TGC AGC TCT GTA TTA CTT TGT CAT TTC CTG TTG TCT CAC TCC TGA GGG					
1521	1530	1539	1548	1557	1566
CTC CTG CAG TAA CTC TGT ACT TCT CTA TCT GCA CAC ACA AAA TGC CCA AGG CAC					
1575	1584	1593	1602	1611	1620
TCA CTG GGG AGG AAG CAA GGA AGC AAA CAG TCT GAG GAA ATG ATG CAA GAA AAT					
1629	1638	1647	1656	1665	1674
CAA ATG GGA ATC TGG GGA CCC AAC ACA ACA TCC TGA AGA TTA TTA AAA GGA AAA					
1683	1692	1701	1710	1719	1728
GAT GCT GAT TGG TAC ATA AAT CTT TTA CAT GGC CTT GGT CTA GAG GAG GCA GGC					
1737	1746	1755	1764	1773	1782
TTT TAG AAT CAT GTT TTG TTA ATC CGC TTC ACT AAA TTG GAC CTT CAC ATA TCT					
1791	1800	1809	1818	1827	1836
AAA AAG CTC TGA AGT GTT TGT ATA TTT GAA ATA CCT CAA TAA AGA GAG AGC TCA					
TTG ACT GT 3'					

FIGURE 1C

1	M	T	C	C	L	P	A	L	R	F	I	A	T	P	R	L	S	A	M	P	H	I	D	N	D	V	K	L	D	F	K	D	V	L	R	P	K	R	S	HQMR		
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	I	E	D	L	K	L	G	F	K	D	V	L	I	R	P	K	R	S	9473772		
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	R	I	D	A	D	L	K	L	D	F	K	D	V	L	L	R	P	K	R	S	9544455
23	T	L	K	S	R	S	E	V	D	L	T	R	S	F	S	F	R	N	S	K	Q	T	Y	S	G	V	P	I	I	A	A	N	M	D	T	V	G	T	F	E	HQMR	
22	T	L	K	S	R	S	D	V	E	L	E	R	Q	F	T	F	K	H	S	G	Q	S	W	S	G	V	P	I	I	A	A	N	M	D	T	V	G	T	F	S	9473772	
23	S	L	K	S	R	A	E	V	D	L	E	R	T	F	T	F	R	N	S	K	O	T	Y	S	G	I	P	I	I	V	A	N	M	D	T	V	G	T	F	E	9544455	
61	M	A	K	V	L	C	K	F	S	L	F	T	A	V	H	K	H	Y	S	L	V	Q	W	Q	E	F	A	G	O	N	P	-	D	C	L	E	H	L	A	HQMR		
62	M	A	S	A	L	A	S	E	D	I	L	T	A	V	H	K	H	Y	S	V	E	E	W	O	A	F	I	N	N	S	S	A	D	V	L	K	H	V	M	9473772		
63	M	A	A	V	M	S	Q	H	S	M	F	T	A	I	H	K	H	Y	S	L	D	D	W	K	L	F	A	T	N	H	P	-	E	C	L	Q	N	V	A	9544455		
102	S	S	G	T	G	S	S	D	F	E	Q	L	E	Q	I	L	E	A	I	P	O	V	K	Y	I	C	L	D	V	A	N	G	Y	S	E	H	F	V	E	F	HQMR	
102	S	T	G	T	S	D	A	D	F	E	K	T	K	Q	I	L	D	N	P	A	L	N	F	V	C	I	D	V	A	N	G	Y	S	E	H	F	V	Q	F	9473772		
102	S	S	G	S	G	Q	N	D	L	E	K	M	T	S	I	L	E	A	V	P	O	V	K	F	I	C	L	D	V	A	N	G	Y	S	E	H	F	V	E	F	9544455	
142	V	K	D	V	R	K	R	F	P	Q	H	T	I	M	A	G	N	V	T	G	E	M	V	E	E	L	I	L	S	G	A	D	I	I	K	V	G	I	G	HQMR		
142	V	A	K	A	R	E	A	W	P	T	K	T	I	C	A	G	N	V	T	G	E	M	C	E	E	L	I	L	S	G	A	D	I	V	K	V	G	I	G	9473772		
142	V	K	L	V	R	A	K	F	P	E	H	T	I	M	A	G	N	V	T	G	E	M	V	E	E	L	I	L	S	G	A	D	I	I	K	V	G	V	G	9544455		
200	P	G	S	V	C	T	T	R	K	K	T	G	V	G	Y	P	Q	L	S	A	V	M	E	C	A	D	A	A	H	G	L	K	G	H	I	I	S	D	G	G	HQMR	
182	P	G	S	V	C	T	T	R	V	K	T	G	V	G	Y	P	Q	L	S	A	V	I	E	C	A	D	A	A	H	G	L	G	G	M	I	V	I	S	D	G	9473772	
182	P	G	S	V	C	T	T	R	T	K	T	G	V	G	Y	P	Q	L	S	A	V	I	E	C	A	D	S	A	H	G	L	K	G	H	I	I	S	D	G	G	9544455	
240	C	S	C	P	G	D	V	A	K	A	F	G	A	G	A	D	F	V	M	L	G	M	L	A	G	H	S	E	S	G	G	E	L	I	E	R	D	G	K	HQMR		
222	C	T	T	P	G	D	V	A	K	A	F	-	A	R	A	D	F	V	M	L	G	M	L	A	G	H	E	E	S	G	G	R	I	V	E	E	N	G	E	9473772		
222	C	T	C	P	G	D	V	A	K	A	F	G	A	G	A	D	F	V	M	L	G	M	F	S	G	H	T	E	C	A	G	E	V	F	E	R	N	G	R	9544455		

FIGURE 2A

280	K	Y	K	L	F	Y	G	M	S	S	E	M	A	M	K	K	Y	A	G	G	V	A	E	Y	R	A	S	E	G	K	T	V	E	V	P	F	K	G	D	V	HOMER
261	K	F	M	L	F	Y	G	M	S	S	E	S	A	M	K	R	H	V	G	G	V	A	E	Y	R	A	A	E	G	K	T	V	K	L	P	L	R	G	P	V	g473772
262	K	L	K	L	F	Y	G	M	S	S	D	T	A	M	N	K	H	A	G	G	V	A	E	Y	R	A	S	E	G	K	T	V	E	V	P	Y	K	G	D	V	g544455
320	E	H	T	I	R	D	I	L	G	G	I	R	S	T	C	T	Y	V	G	A	A	K	L	K	E	L	S	R	R	T	T	F	I	R	V	T	O	Q	V	N	HOMER
301	E	N	T	A	R	D	I	L	G	G	L	R	S	A	C	T	Y	V	G	A	S	R	L	K	E	L	T	K	R	T	T	F	I	R	V	O	E	Q	E	N	g473772
302	E	N	T	I	L	D	I	L	G	G	L	R	S	T	C	T	Y	V	G	A	A	K	L	K	E	L	S	R	R	A	T	F	I	R	V	T	O	H	N	g544455	
360	P	I	F	S	E	A	C																																		HOMER
341	R	I	F	N	N	L																																		g473772	
342	T	V	F	S																																			g544455		

FIGURE 2B

The graph displays a single data series as a continuous black line. The vertical axis (y-axis) is labeled with values -2, -1, 0, 1, and 2. The horizontal axis (x-axis) is labeled with values 1, 70, 139, 208, 277, and 346. The signal begins at a value of about 0.8 at x=1, drops below zero around x=20, reaches a local minimum of approximately -0.8 at x=50, and then rises to a local maximum of about 0.8 at x=100. From x=100 to x=346, the signal fluctuates rapidly around the zero line, with peaks reaching approximately 0.8 and troughs reaching approximately -0.8.

FIGURE 3B

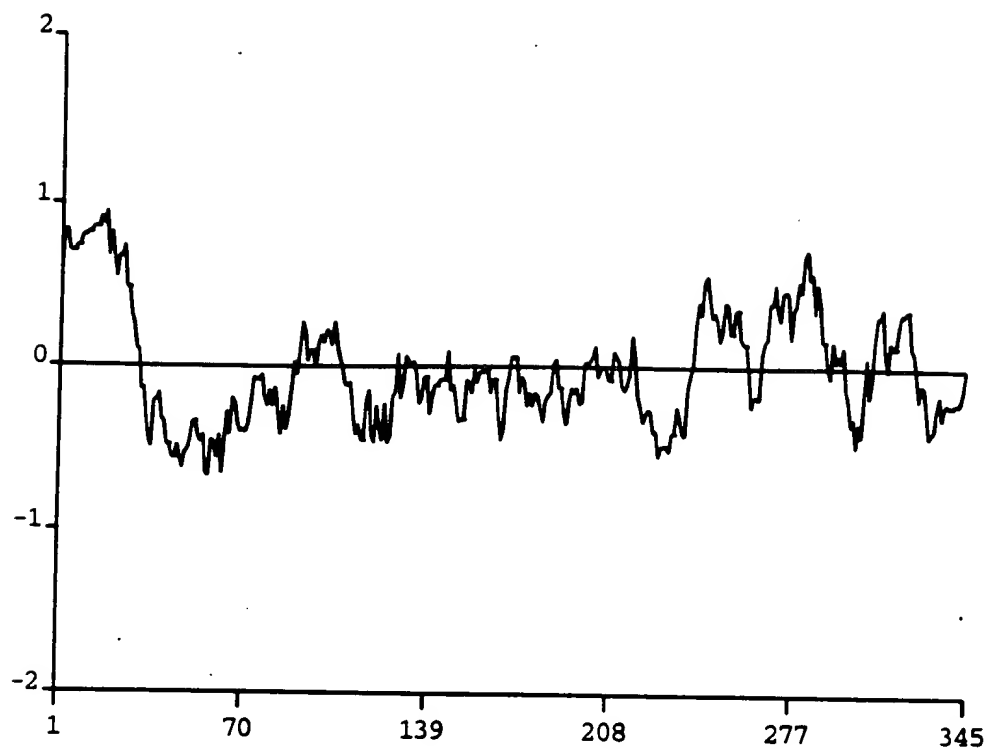


FIGURE 3C

Library	Lib Description	Abun	Pct Abun
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	1	0.0332
ENDCNOT03	endothelial cells, dermal microvascular, neonatal M	1	0.0210
LUNGFEM01	lung, fetal, NORM, WM	1	0.0148
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0117
BRAINOT09	brain, fetal M	1	0.0093
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0075

FIGURE 4